



## Raw Sequence Listing Error Summary

<u>PATENT OFFICE</u> <u>SEARCHED</u> <u>INDEXED</u> <u>MAILED</u>	<u>ERROR DETECTED</u>	<u>SUGGESTED CORRECTION</u>	<u>SERIAL NUMBER:</u> <u>09/180798</u>
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE			
1	____ Wrapped Nucleic	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3, as this will prevent "wrapping".	
2	____ Wrapped Aminos	The amino acid number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3, as this will prevent "wrapping".	
3	____ Incorrect Line Length	The rules require that a line not exceed 72 characters in length. This includes spaces.	
4	____ Misaligned Amino Acid Numbering	The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.	
5	____ Non-ASCII	This file was not saved in ASCII (DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text so that it can be processed.	
6	____ Variable Length	Sequence(s) ____ contain n's or Xaa's which represented more than one residue. As per the rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.	
7	____ PatentIn ver. 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence.	
8	____ Skipped Sequences (OLD RULES)	Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS") (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: This sequence is intentionally skipped  Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).	
9	____ Skipped Sequences (NEW RULES)	Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence. <210> sequence id number <400> sequence id number 000	
10	____ Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Use of <220> to <223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.	
11	____ Use of <213>Organism (NEW RULES)	Sequence(s) ____ are missing this mandatory field or its response.	
12	____ Use of <220>Feature (NEW RULES)	Sequence(s) ____ are missing the <220>Feature and associated headings. Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown" Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)	
13	____ PatentIn ver. 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other means to copy file to floppy disk.	